0240

# RAW SEQUENCE LISTING
## ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
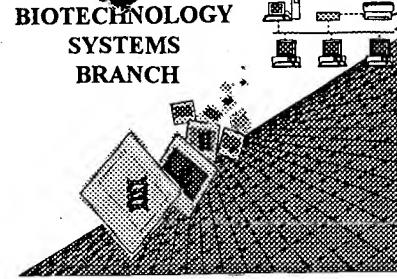BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/591,466_

Source: _OIPE_

Date Processed by STIC: _6/16/2000_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**

2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
**http://www.uspto.gov/web/offices/pac/checker**

<u>ERROR DETECTED</u>   <u>SUGGESTED CORRECTION</u>                      SERIAL NUMBER: _O 9/S 91,466_

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
                           This may occur if your file was retrieved in a word processor after creating it.
                           Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos     The amino acid number/text at the end of each line "wrapped" down to the next line.
                           This may occur if your file was retrieved in a word processor after creating it.
                           Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
        Numbering               between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII          This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
                           Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length    Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
                           As per the rules, each n or Xaa can only represent a single residue.
                           Please present the maximum number of each residue having variable length and
                           indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
                           sequence(s) _____. Normally, PatentIn would automatically generate this section from the
                           previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
                           to the subsequent amino acid sequence.

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
        (OLD RULES)         (2) INFORMATION FOR SEQ ID NO:X:
                            (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
                            (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
                            **This sequence is intentionally skipped**

                            Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
        (NEW RULES)         **<210>  sequence id number**
                            **<400>  sequence id number**
                            **000**

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
        (NEW RULES)         Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
                            In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
        (NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
        (NEW RULES)         Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
                            **Please explain source of genetic material in <220> to <223> section.**
                            (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted
                            file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
                            Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION  *US/09/591,466*

DATE: 06/17/2000
TIME: 06:59:40

*INPUT SET: S35638.raw*

This Raw Listing contains the General
Information Section and up to the first 5 pages.

*see item 5 on Exa Summary sheet*

Does Not Comply
Corrected Diskette Needed

```
 1                               SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5        (i) APPLICANT:  ↑ more exp - all responses must be on same line as heading
 6        (A) NAME: von Schaewen, Antje Dr. rer. nat.
 7        (B) STREET: Natruperstrasse 169a
 8        (C) CITY: Osnabrueck
 9        (E) COUNTRY: Germany
10        (F) POSTAL CODE (ZIP): D-49076
11        (G) TELEPHONE: +49-541-684029
12
13        (ii) TITLE OF INVENTION: Plant gntI sequences and the use thereof for the produ
14
15        (iii) NUMBER OF SEQUENCES: 6
16
17  (√)   (iv) COMPUTER READABLE FORM:
18        (A) MEDIUM TYPE: Floppy disk
19        (B) COMPUTER: IBM PC compatible
20        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
21        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
22
23    (2) INFORMATION FOR SEQ ID NO: 1:
24
25        (i) SEQUENCE CHARACTERISTICS:
26        (A) LENGTH: 1669 base pairs
27        (B) TYPE: nucleic acid
28        (C) STRANDEDNESS: double
29        (D) TOPOLOGY: linear
30
31        (ii) MOLECULE TYPE: cDNA to mRNA
32
33        (iii) HYPOTHETICAL: NO
34
35        (iv) ANTI-SENSE: NO
36
37        (vi) ORIGINAL SOURCE:
38        (A) ORGANISM: Solanum tuberosum
39        (B) STRAIN: Desiree
40        (D) DEVELOPMENTAL STAGE: Sink organ
41        (F) TISSUE TYPE: Mesophyll
42        (G) CELL TYPE: Leaf cells
43
44        (vii) IMMEDIATE SOURCE:
45        (A) LIBRARY: Lambda ZAP II (Eco RI)
46        (B) CLONE: gntI-A1(K)
```

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

(v) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

*all text must be visible*

*add these mandatory headings and responses for a U.S. filing*

*add these mandatory headings*

*EPO format of PatentIn is invalid for a U.S. case*

*see following pages*

09/591,466

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS: 446
      (A) LENGTH: 447 amino acids 446
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

*see next page*

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val
 1               5                  10                  15

Ala Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln
                20                  25                  30

Ser Glu Tyr Val Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His
                35                  40                  45

Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln
        50                  55                  60

Gly Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu
65                  70                  75                  80

Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
                85                  90                  95

Lys Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val
            100                 105                 110

Met Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile
            115                 120                 125

Leu Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
    130                 135                 140

Gln Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly
145                 150                 155                 160

Gln Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu
                165                 170                 175

Arg Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
            180                 185                 190

Trp Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile
            195                 200                 205

Ile Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe
    210                 215                 220

Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
225                 230                 235                 240

Ser Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp
                245                 250                 255
```

Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
         260              265             270

Lys Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
         275            280          285

Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
         290            295          300

Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
305            310          315          320

Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
         325            330          335

Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp
         340            345          350

Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile
         355            360          365

His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val
         370            375          380

Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln
385            390          395          400

Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr
         405            410          415

Lys Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu
         420            425          430

Val Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr
         435            440          445

(*) delete ending stop codon

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS: 446
       (A) LENGTH: 447 amino acids
       (B) TYPE: amino acid
       (D) TOPOLOGY: linear

*see next page*

   (ii) MOLECULE TYPE: protein
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

```
Met Arg Gly Asn Lys Phe Cys Cys Asp Phe Arg Tyr Leu Leu Ile Leu
 1               5               10              15

Ala Ala Val Ala Phe Ile Tyr Thr Gln Met Arg Leu Phe Ala Thr Gln
            20              25              30

Ser Glu Tyr Ala Asp Arg Leu Ala Ala Ile Glu Ala Glu Asn His
        35              40              45

Cys Thr Ser Gln Thr Arg Leu Leu Ile Asp Gln Ile Ser Leu Gln Gln
    50              55              60

Gly Arg Ile Val Ala Leu Glu Glu Gln Met Lys Arg Gln Asp Gln Glu
65              70              75              80

Cys Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile
            85              90              95

Lys Lys Leu Ile Gly Asn Val Gln Met Pro Val Ala Ala Val Val Val
            100             105             110

Met Ala Cys Asn Arg Ala Asp Tyr Leu Glu Lys Thr Ile Lys Ser Ile
        115             120             125

Leu Lys Tyr Gln Ile Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser
    130             135             140

Gln Asp Gly Ser His Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Asp
145             150             155             160

Gln Leu Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val His Thr Glu
            165             170             175

Arg Pro Gly Glu Leu Ile Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys
        180             185             190

Trp Ala Leu Asp Gln Leu Phe Tyr Lys His Asn Phe Ser Arg Val Ile
    195             200             205

Ile Leu Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Phe Phe
    210             215             220

Glu Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile
225             230             235             240

Ser Ser Trp Asn Asp Asn Gly Gln Met Gln Phe Val Gln Asp Pro Tyr
            245             250             255
```

Ala Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser
260 265 270

Lys Ser Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp
275 280 285

Asp Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile
290 295 300

Arg Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser
305 310 315 320

Leu Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp
325 330 335

Val Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp
340 345 350

Asn Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile
355 360 365

His Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val
370 375 380

Arg Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asn Ile Ala Arg Gln
385 390 395 400

Phe Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr
405 410 415

Lys Gly Ile Val Val Phe Arg Tyr Gln Thr Ser Arg Arg Val Phe Leu
420 425 430

Val Gly His Asp Ser Leu Gln Gln Leu Gly Ile Glu Asp Thr
435 440 445

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 445 amino acids
       (B) TYPE: Amino acid
       (D) TOPOLOGY: Linear

    (ii) MOLECULE TYPE: Protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Ala Arg Ile Ser Cys Asp Leu Arg Phe Leu Leu Ile Pro Ala Ala
1               5                   10                  15

Phe Met Phe Ile Tyr Ile Gln Met Arg Leu Phe Gln Thr Gln Ser Gln
            20                  25                  30

Tyr Ala Asp Arg Leu Ser Ser Ala Ile Glu Ser Glu Asn His Cys Thr
            35                  40                  45

Ser Gln Met Arg Gly Leu Ile Asp Glu Val Ser Ile Lys Gln Ser Arg
        50                  55                  60

Ile Val Ala Leu Glu Asp Met Lys Asn Arg Gln Asp Glu Glu Leu Val
65                  70                  75                  80

Gln Leu Lys Asp Leu Ile Gln Thr Phe Glu Lys Lys Gly Ile Ala Lys
                85                  90                  95

Leu Thr Gln Gly Gly Gln Met Pro Val Ala Ala Val Val Val Met Ala
            100                 105                 110

Cys Ser Arg Ala Asp Tyr Leu Glu Arg Thr Val Lys Ser Val Leu Thr
        115                 120                 125

Tyr Gln Thr Pro Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln Asp
    130                 135                 140

Gly Ser Asp Gln Ala Val Lys Ser Lys Ser Leu Ser Tyr Asn Gln Leu
145                 150                 155                 160

Thr Tyr Met Gln His Leu Asp Phe Glu Pro Val Val Thr Glu Arg Pro
                165                 170                 175

Gly Glu Leu Thr Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp Ala
            180                 185                 190

Leu Asp Gln Leu Phe Tyr Lys His Lys Phe Ser Arg Val Ile Ile Leu
        195                 200                 205

Glu Asp Asp Met Glu Ile Ala Pro Asp Phe Phe Asp Tyr Phe Glu Ala
    210                 215                 220

Ala Ala Ser Leu Met Asp Arg Asp Lys Thr Ile Met Ala Ala Ser Ser
225                 230                 235                 240

Trp Asn Asp Asn Gly Gln Lys Gln Phe Val His Asp Pro Tyr Ala Leu
                245                 250                 255
```

```
Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Lys Arg Ser
        260             265             270

Thr Trp Asp Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp Asp
        275             280             285

Trp Leu Arg Leu Lys Glu Asn His Lys Gly Arg Gln Phe Ile Ala Pro
        290             295             300

Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu Gly
305             310             315             320

Gln Phe Phe Ser Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val Thr
        325             330             335

Val Asp Trp Lys Ala Lys Asp Leu Gly Tyr Leu Thr Glu Gly Asn Tyr
        340             345             350

Thr Lys Tyr Phe Ser Gly Leu Val Arg Gln Ala Arg Pro Ile Gln Gly
        355             360             365

Ser Asp Leu Val Leu Lys Ala Gln Asn Ile Lys Asp Asp Asp Arg Ile
    370             375             380

Arg Tyr Lys Asp Gln Val Glu Phe Glu Arg Ile Ala Gly Glu Phe Gly
385             390             395             400

Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Thr Ala Tyr Lys Gly
            405             410             415

Val Val Val Phe Arg Ile Gln Thr Thr Arg Arg Val Phe Leu Val Gly
            420             425             430

Pro Asp Ser Val Met Gln Leu Gly Ile Arg Asn Ser *  delete
        435             440         4/5
```